

01/11

APPENDIX 100 FIG
3
DRAFTSMAN

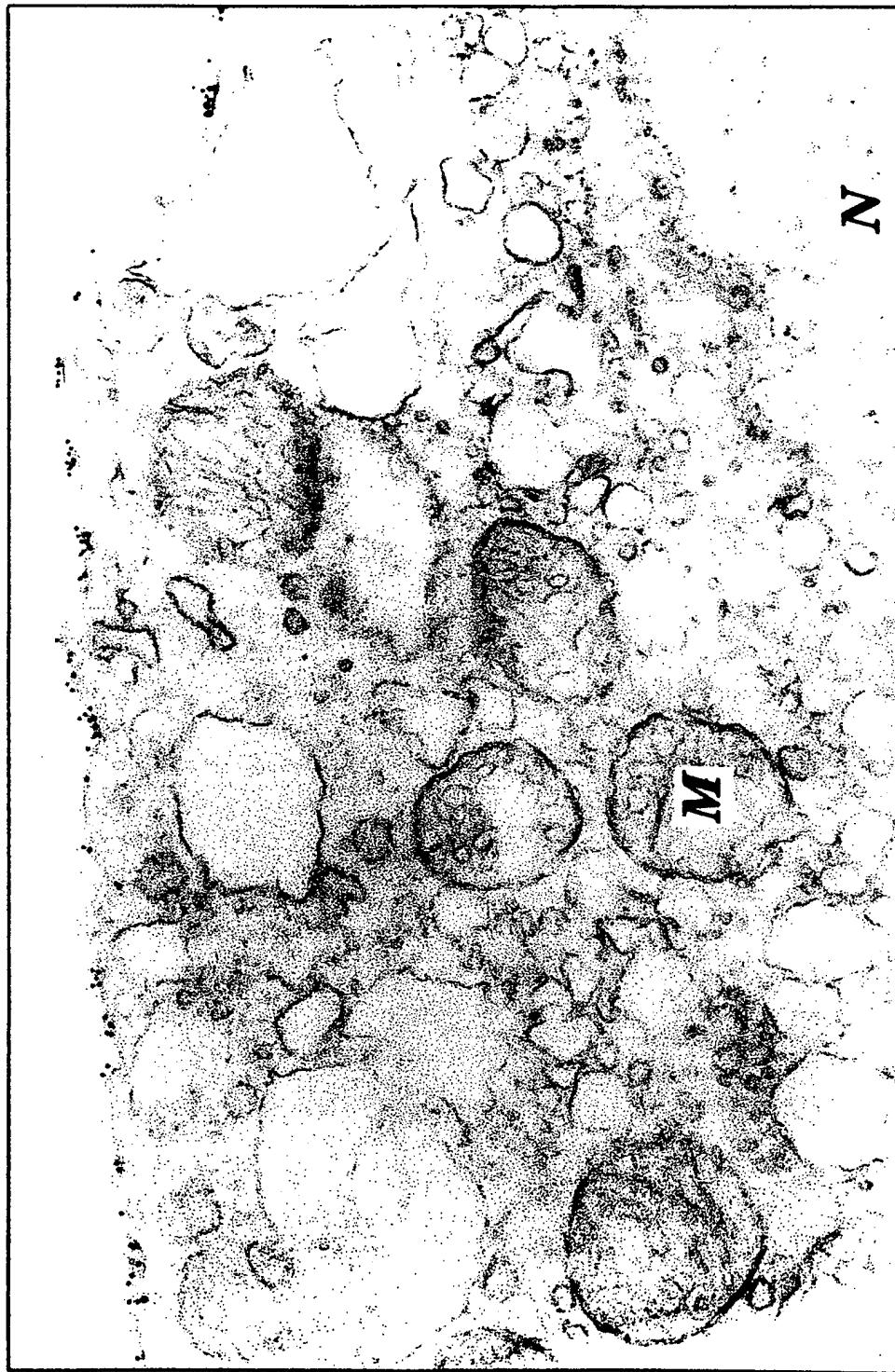


FIG. 1

02/11

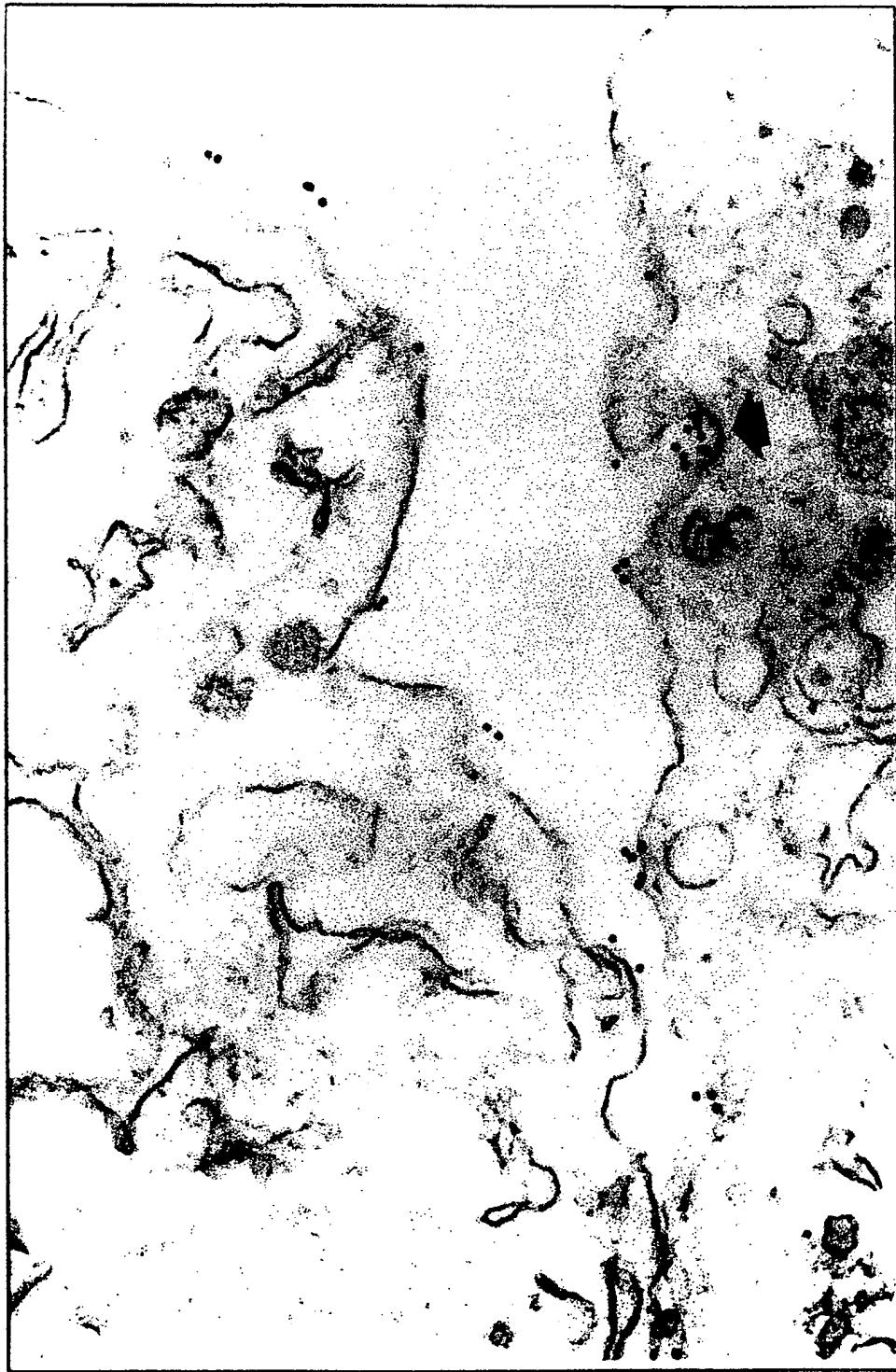
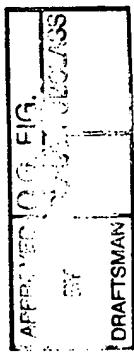


FIG. 2

03/11

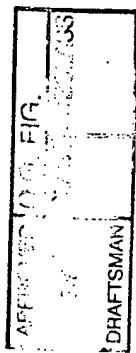


FIG. 3

04/11

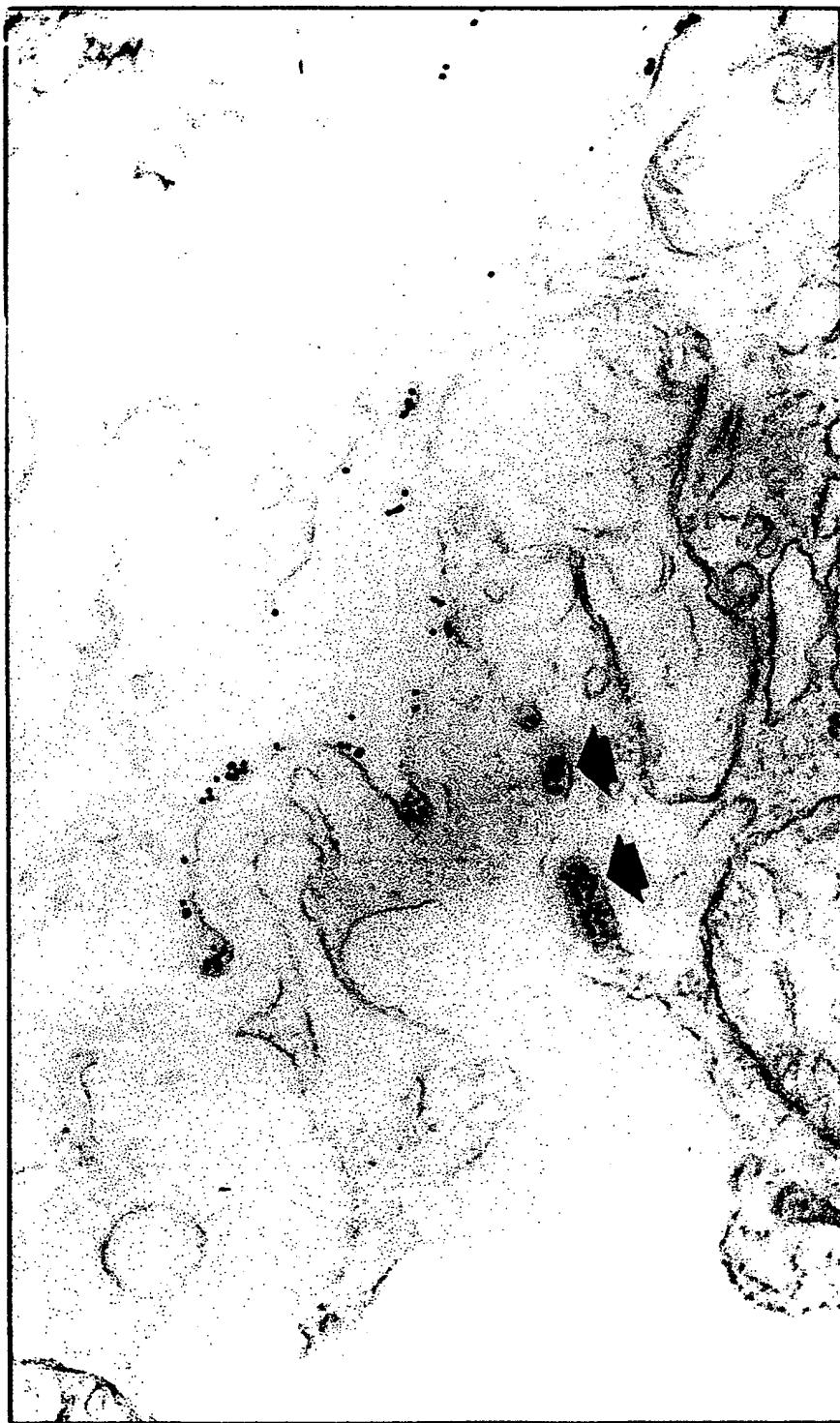


FIG. 4

44-11111-11111-11111
111111111111111111111111
DRAFTSMAN

05/11

DRAFTSMAN

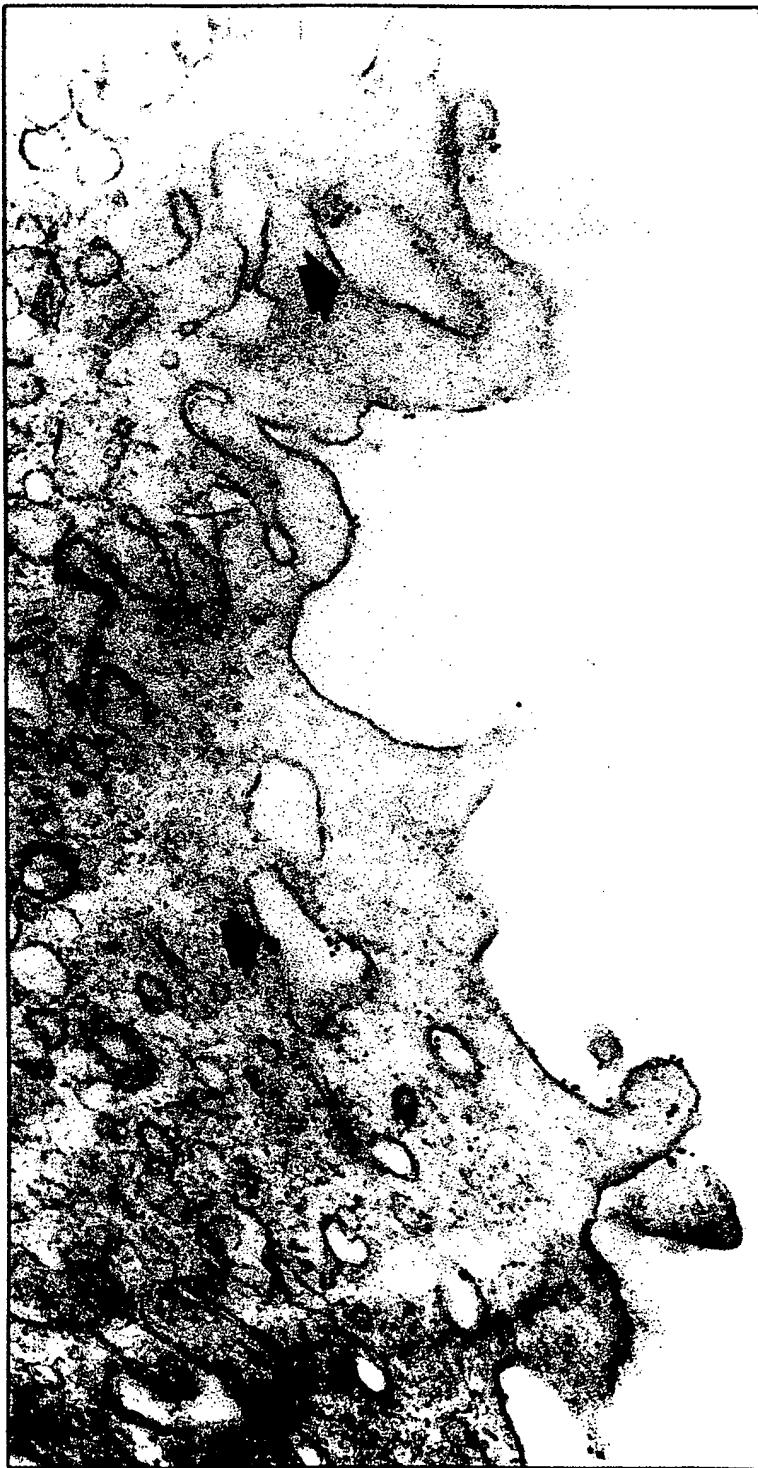


FIG. 5

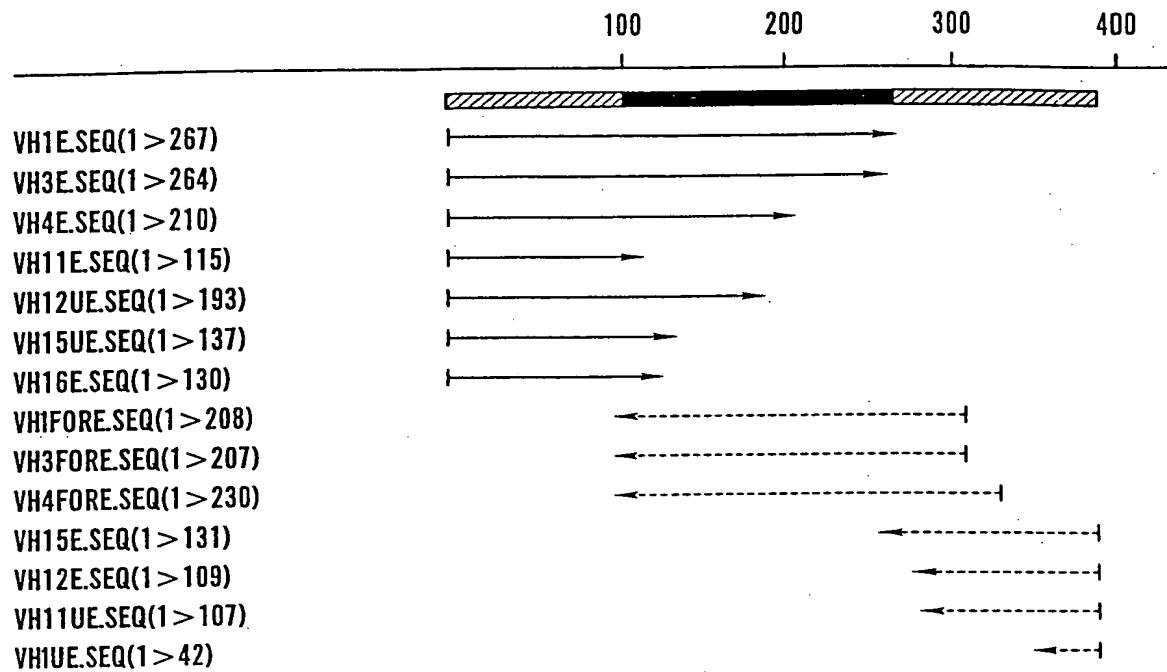
TREATMENT AND DIAGNOSIS OF PROSTATE CANCER

INV: N. BANDER

SN: 09/357,704

06/11

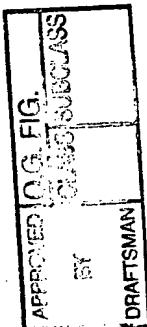
APPROVED	O. G. FIG.
SPEC.	CLASS
SPEC.	SUBCLASS
DRAFTSMAN	

**FIG. 6**

07/11

ENZYMES: ALL 74 ENZYMES (NO FILTER)

SETTINGS: LINEAR, CERTAIN SITES ONLY, STANDARD GENETIC CODE



SEQ. ID.NO. 1 TCTCCTGTCAGGAACCTGCAGGTGTCCTCTCTGAGGTCCAGCTGCAACAGTCGGACCTGAACTGGTGAAG 70
 SEQ. ID.NO. 2 AGAGGACAGTCCTTGACGTCACAGGAGAGACTCCAGGTGAGGTGTCAGACCTGACTGACACTTC
 SEQ. ID.NO. 3 S P V R N C R C P L . G P A A T V W T . T G E
 SEQ. ID.NO. 4 L L S G T A G V L S E V Q L Q Q S G P E L V K
 SEQ. ID.NO. 5 L S C Q E L Q V S S L R S S C N S L D L N W . S

Pst I | Dde I | Ava II | Alu I | Ava II | Eco57 I
 Sau96 I | Sau96 I | Pvu II | Sau96 I | Bsr I

Hph I | Bsp6 II | EcoRV | Dra III | Bsr I

SEQ. ID.NO. 1 CCTGGGACTTCAGTGAGGATATCTGCAAGACTCTGGATAACACATTCACTGAATAACCAACACTGGG 140
 SEQ. ID.NO. 2 GGACOCTGAAGTCACCTCTATAGGAGCTCTGAAGACCTATGTTGAAAGTACCTATAATGGTATGTGACCC
 SEQ. ID.NO. 3 A W D F S E D I L Q D F W I H I H . I Y H T L G
 SEQ. ID.NO. 4 P G T S V R I S C K T S G Y T F T E Y T I H W
 SEQ. ID.NO. 5 L G L Q . G Y P A R L L D T H S L N T P Y T G

Hph I | Nco I | Rsa I | Kpn I

SEQ. ID.NO. 1 TGAAGCAGAGCCATGGAAAGAGCCCTTGAGTGGATGGAAACATCAATCTAACAAATGGTGGTACACCTA 210
 SEQ. ID.NO. 2 ACTTOGTCCTGGTACCTTCTGGAACTCACTAACCTTGTAGTTAGGATTTGTTACCAACATGGTGGAT
 SEQ. ID.NO. 3 E A E P W K E P . V D W K H Q S . Q W W Y H L
 SEQ. ID.NO. 4 V K Q S H G K S L E W I G N I N P N N G G T T Y
 SEQ. ID.NO. 5 S R A M E R A L S G L E T S I L T M V V P P

Taq I | Hae III | Acc I | Bsr I | Rsa I | Alu I | Ban II | Sac I

SEQ. ID.NO. 1 CAATCAGAAGTCTGAGGACAAGGCCACATTGACTCTGAGACAAGTCCTCCAGTACAGCCTACATGGAGCTC 280
 SEQ. ID.NO. 2 GTTGTCTCAAGCTCTGTCGGTGTAACTGACATCTGTCAGGAGGTCATGTCGGATGACCTCGAG
 SEQ. ID.NO. 3 Q S E V R G Q G H I D C R Q V L Q Y S L H G A
 SEQ. ID.NO. 4 N Q K F E D K A T L T V D K S S S T A Y M E L
 SEQ. ID.NO. 5 T I R S S R T R P H . L . T S P P V Q P T W S S

Dde I | Hinf I | Pst I | Alu I | Pvu II | Sau96 I | Bsr I | Hae III

SEQ. ID.NO. 1 CGCAGCCTAACATCTGAGGATTCTGAGCTCTATATGTCAGCTGGTGGAACTTTGACTACTGGGGCC 350
 SEQ. ID.NO. 2 GCGTGGATTGTAGACTCTAACAGCTCAGATAATAACACGTCGGACCAACCTGAAACTGATGACCCCG
 SEQ. ID.NO. 3 P Q P N I . G F C S L L L C S W L E L . L L G P
 SEQ. ID.NO. 4 R S L T S E D S A V Y Y C A A G W N F D Y W G
 SEQ. ID.NO. 5 A A . H L R I L Q S I I V Q L V G T L T T G A

Alw26 I | Dde I

SEQ. ID.NO. 1 AAGGCACCAACTCACAGTCCTCAGCCAAAAGACACCC
 SEQ. ID.NO. 2 TTCCGTGGTGAAGAGCTGTCAGAGGAGTCGGTTTGTGTCGGG 391
 SEQ. ID.NO. 3 R H H S H S L L S Q N D T
 SEQ. ID.NO. 4 Q G T T L T V S S A K T T P
 SEQ. ID.NO. 5 K A P L S Q S P Q P K R H P

FIG. 7

08/11

APPROVED	O. G. FIG.
CLASS	100-1000 SUBCLASS
BY	
DRAFTSMAN	

LIPMAN-PEARSON PROTEIN ALIGNMENT
KTUPLE: 2; GAP PENALTY: 4; GAP LENGTH PENALTY: 12

SEQ1(1>115) J591VH.PRO (1>115)	SEQ2(1>125) MUVHIIA.PRO (1>125)	SIMILARITY INDEX 75.6	GAP NUMBER 2	GAP LENGTH 10	CONSENSUS LENGTH 125
--------------------------------------	---------------------------------------	--------------------------	-----------------	------------------	-------------------------

EVQLQQSGPELVKPGTSVRISCKTSGYTFTEYTI-HWVKQSHGKSLEWIGNINPNNGTT
 EVQLQQSGPELVKPG:SV:ISCK:SGYTF:Y: :WVKQS.GKSLEWIG:INP.NGTT:
 EVQLQQSGPELVKPGASVKISCKASGYTFDYYMNINWVKOSPGKSLEWIGDINPGNGTS
 YNQKFEDKAILTVDKSSSTAYMELRSLTSEDSAVYYCAAG-----WNFDYWGQGTT
 YNQKF.:KATLTVDKSSSTAYM:L.SLTSEDSAVYYCA G ..FDYWGQGTT
 YNQKFKGKAILTVDKSSSTAYMQLSSLTSEDSAVYYCARGYYSSSYMAYYAFDYWGQGTT
 LTVSS
 :TVSS
 VTVSS

FIG. 8

TREATMENT AND DIAGNOSIS OF PROSTATE CANCER

INV: N. BANDER

SN: 09/357,704

09/11

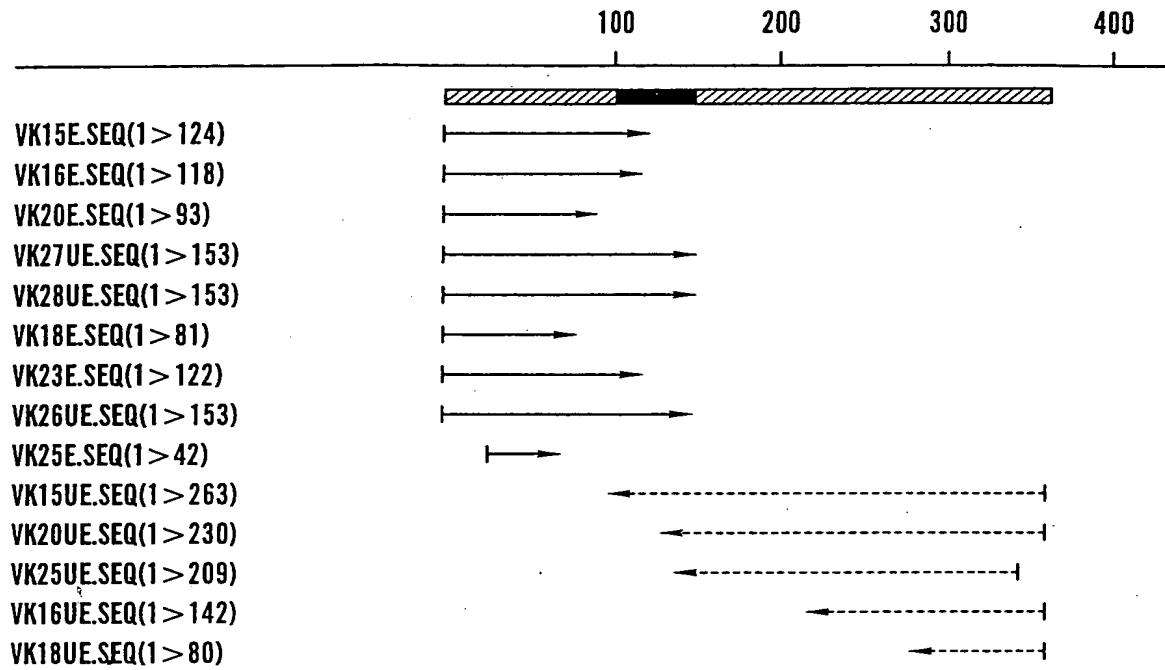
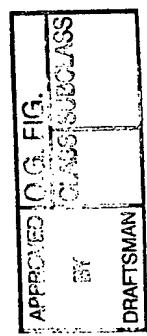


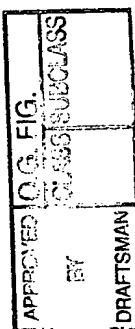
FIG. 9

TREATMENT AND DIAGNOSIS OF PROSTATE CANCER

INV: N. BANDER

SN: 09/357,704

10/11



ENZYMES: ALL 74 ENZYMES (NO FILTER)
 SETTINGS: LINEAR, CERTAIN SITES ONLY, STANDARD GENETIC CODE

Alu | Hph I
 SEQ. ID. NO. 9 T T A T A T G G A G C T G A T G G G A A C A T T G T A A T G A C C C A A T C T C C C A A T C C A T G T C C A T G T C A G T A G G G A G A G A 70
 SEQ. ID. NO. 10 A A T A T A C C T O G A C T A C C C T T G T A A C A T T A C T G G G T T A G A G G G T T A G G T A C A G G T A C A G T C A T C C T C T C T
 SEQ. ID. NO. 11 L Y G A D G N I V M T Q S P K S M S M S V G E
 SEQ. ID. NO. 12 Y M E L M G T L . . P N L P N P C P C Q . E R
 SEQ. ID. NO. 13 I I W S . . W E H C N D P I S Q I H V H V H V S R R E

Hae III | Bsr I
 SEQ. ID. NO. 9 G G G T C A C C T T G A C C T G C A A G G C C A G T G A G A A T G T G G T T A C T T A G T T C C T G G T A C A C A G A A A C C A G A 140
 SEQ. ID. NO. 10 C C C A G T G G A C T G G A O G T C C C G T C A C T C T T A C A C C A A T G A A T A C A A A G G A C C A T A G T T G T C T T T G G T C T
 SEQ. ID. NO. 11 R V T L T C K A S E N V V T Y V S W Y Q Q K P E
 SEQ. ID. NO. 12 G S P . P A R P V R M W L L M F P G I N R N Q
 SEQ. ID. NO. 13 G H L D L Q G Q . E C G Y L C F L V S T E T R

Alw26 I | Fok I | Hpa II | Rsa I | Ava II | Mbo I | Bsr I | Sau96 I | Dpn I | Bsa0 I | Pvu I
 SEQ. ID. NO. 9 G C A G T C T C C T T A A A C T G C T G A T A T A C G G G C A T C C A A C C G G T A C A C T G G G T T C C C C G A T G C T C A C A G G C 210
 SEQ. ID. NO. 10 C G T C A G A G G A T T T G A C G A C T T A T G C C C C G T A G G T T G G C C A T G T G A C C C C A G G G G C T A G G G A A G T G T C C G
 SEQ. ID. NO. 11 Q S P K L L I Y G A S N R Y T G V P D R F T G
 SEQ. ID. NO. 12 S S L L N C . Y T G H P T G T L G S P I A S Q A
 SEQ. ID. NO. 13 A V S . T A D I R G I Q P V H W G P R S L H R

Mbo I | Dpn I | Bsp6 II | Mbo II | Ec057 I
 SEQ. ID. NO. 9 A G T G G A T C T G C A A C A G A T T T C A C T C T G A C C A T C A G C A G T T G C A G G G T G A A G A C C T T G C A G A T T A T C A T T 280
 SEQ. ID. NO. 10 T C A C C T A G A O G T G T C T A A A G T G A G A C T G G T A G T G T C A C A C G T C O G A C T T C T G G A A C G T C T A A T A G T G A
 SEQ. ID. NO. 11 S G S A T D F T L T I S S V Q A E D L A D Y H
 SEQ. ID. NO. 12 V D L Q Q I S L . P S A V C R L K T L Q I I T
 SEQ. ID. NO. 13 Q W I C N R F H S D H Q Q C A G . R P C R L S L

Ava II | Alu I | Rsa I | Sau96 I | Alu I
 SEQ. ID. NO. 9 G T G G A C A C G G T T A C A G C T A T C C G T A C A C G T T C G G A G G G G G A C C A A G C T G G A A A T A A A C C G G C T G A T G C 350
 SEQ. ID. NO. 10 C A C C T G T C C C A A T G T G O G A T A G G C A T G T G C A A G C C T T C C C C C T G G T T C G A C C T T T A T T T G C C C G A C T A G G
 SEQ. ID. NO. 11 C G Q G Y S Y P Y T F G G G T K L E I K R A D A
 SEQ. ID. NO. 12 V D R V T A I R T R S E G G P S W K . N G L M
 SEQ. ID. NO. 13 W T G L Q L S V H V R R G D Q A G N K T G . . C

SEQ. ID. NO. 9 T G C A C C A A C T G T A
 SEQ. ID. NO. 10 A C G T G G G T G A C A T
 SEQ. ID. NO. 11 A P T V
 SEQ. ID. NO. 12 L H Q L Y
 SEQ. ID. NO. 13 C T N C

363

FIG. 10

TREATMENT AND DIAGNOSIS OF PROSTATE CANCER

INV: N. BANDER

SN: 09/357,704

11/11

APPROVED	C. S. FIG.
BY	CLASS
DRAFTSMAN	

LIPMAN-PEARSON PROTEIN ALIGNMENT
KTUPLE: 2; GAP PENALTY: 4; GAP LENGTH PENALTY: 12

SEQ1(1>107) J591VK.PRO (1>107)	SEQ2(1> 1 1 1) MUVKV.PRO (1>109)	SIMILARITY INDEX 60.4	GAP NUMBER 2	GAP LENGTH 2	CONSENSUS LENGTH 109
--------------------------------------	--	-----------------------------	--------------------	--------------------	----------------------------

NIVMTQSPKMSMSVGERVILTCKAS-ENVVITYVSWYQOKPEQSPKLLIYGA
 :I MTQSP.S:S S:G:RVT:TC:AS ::: .Y: :WYQOKP. SPKLLIY AS. .:GVP
 DIQMTQSPSSILSASLGDRTITCRASQDDISNYLNWYQOKPGGSPKLLIYASRLHSGVP
 ↑ 10 ↑ 20 ↑ 30 ↑ 40 ↑ 50 ↑ 60
 DRFTIGSGSATDFITLTISSVQAEDLADYHCGQGYSY-PYTFGGGTKEIK
 .RF:GSGS:TD: :LTIS:::ED:A.Y C QG : P TFGGGTKEIK
 SRFSGSGSGTDYSLTISNLEQEDIATYFOQQQGNTLPPRTFGGGTKEIK
 ↑ 60 ↑ 70 ↑ 80 ↑ 90 ↑ 100
 ↑ 70 ↑ 80 ↑ 90 ↑ 100

FIG. 11